

SEQUENCE LISTING

<110> Roschke, Viktor
Rosen, Craig A.
Ruben, Steven, M.

<120> Human G-protein Chemokine Receptor (CCR5) HDGNR10

<130> 1488.115000I

<150> PCT/US01/04153
<151> 2001-02-09

<150> 09/779,880
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<150> 60/297,257
<151> 2001-06-12

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<170> PatentIn version 3.1

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Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln
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Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
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Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe
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Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr
275 280 285

Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly
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Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val
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gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180
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cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180
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Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20 25 30
ctg cct ccg ctc tac tca ctg gtg ttc atc ttt ggt ttt gtg ggc aac 144
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35 40 45
atg ctg gtc atc ctc atc ctg ata aac tgc aaa agg ctg aag agc atg 192
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Val	Met 210	Val	Ile	Cys	Tyr	Ser 215	Gly	Ile	Leu	Lys	Thr 220	Leu	Leu	Arg	Cys	
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Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
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130 135 140
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
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Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
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Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
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Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
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Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
210 215 220
Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
225 230 235 240
Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
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Cys	Lys	Cys	Cys	Ser	Ile	Phe	Gln	Gln	Glu	Ala	Pro	Glu	Arg	Ala	Ser
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<210> 56
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23

<210> 57
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Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Asp Trp Ile
35 40 45
Gly Arg Ile Tyr Thr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60
Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Arg Phe Ser Leu
65 70 75 80
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Asp Arg Gly Ser Ser Trp Tyr Pro Asp Ala Phe Asp Ile Trp Gly
100 105 110
Gln Gly Thr Met Val Thr Val Ser Ser
115 120

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1 5 10 15
gaa aga gcc acc ctc tcc tgc agg gcc agt cag cgt gtt acc agc agc 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Thr Ser Ser
20 25 30
tgc tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
Cys Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
atc tat ggt aca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
Ile Tyr Gly Thr Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt agc tca cct 288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Ser Ser Pro
85 90 95
ctc acc ttc ggc caa ggg aca cga ctc gag atc aaa cgt 327
Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
100 105

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1				5					10					15		
tcc	ctt	aga	ctc	tcc	tgt	gca	gcc	tcc	gga	ttc	act	ttc	agt	aac	gcc	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asn	Ala	
			20					25					30			
tgg	atg	acc	tgg	gtc	cgc	cag	gct	cca	ggg	aag	agg	ctg	gag	tgg	gtt	144
Trp	Met	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Arg	Leu	Glu	Trp	Val	
		35					40					45				
ggc	cgt	att	aaa	agc	aat	gct	gat	ggc	ggg	tca	aca	gac	tac	gct	gca	192
Gly	Arg	Ile	Lys	Ser	Asn	Ala	Asp	Gly	Gly	Ser	Thr	Asp	Tyr	Ala	Ala	
	50					55					60					
ccc	gtg	aaa	ggc	aga	ttc	acc	atc	tca	aga	gat	gat	tca	aaa	aac	acg	240
Pro	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	
65					70					75					80	
ctg	tat	ctg	caa	atg	aac	agc	ctg	aaa	acc	gag	gac	aca	gcc	gtg	tat	288
Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr	
				85					90					95		
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379

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Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Phe	Thr	Phe	Ser 30	Asn	Ala
Trp	Met	Thr 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Arg	Leu 45	Glu	Trp	Val
Gly	Arg 50	Ile	Lys	Ser	Asn	Ala 55	Asp	Gly	Gly	Ser	Thr 60	Asp	Tyr	Ala	Ala
Pro 65	Val	Lys	Gly	Arg	Phe 70	Thr	Ile	Ser	Arg	Asp 75	Asp	Ser	Lys	Asn	Thr 80
Leu	Tyr	Leu	Gln	Met 85	Asn	Ser	Leu	Lys	Thr 90	Glu	Asp	Thr	Ala	Val 95	Tyr
Tyr	Cys	Asn	Thr 100	Asp	Lys	Gly	Gly	Ser 105	Tyr	Pro	Tyr	Tyr	Tyr 110	Tyr	Gly
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Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly		
1				5					10					15			
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gac	aga	gtc	acc	atc	act	tgc	cgg	gca	agt	cag	ggc	att	aga	aat	gat	96	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Arg	Asn	Asp		
			20					25					30				
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tta	ggc	tgg	tat	cag	cag	aaa	cca	ggg	aaa	gcc	cct	aag	cgc	ctg	atc	144	
Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Arg	Leu	Ile		
		35					40					45					
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tat	qat	gca	tcc	agt	ttg	caa	agt	ggg	gtc	cca	tca	agg	ttc	agc	ggc	192	

acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agt agt tac 96
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20 25 30

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Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	
1				5					10					15		

gaa	aga	gtc	acc	ctc	tcc	tgc	agg	gcc	agt	cag	aga	ggt	agc	aac	agc	96
Glu	Arg	Val	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Arg	Val	Ser	Asn	Ser	
			20					25					30			

tac	tta	gcc	tgg	tac	cag	cag	aaa	cct	ggc	cag	gct	ccc	agg	ttc	ctc	144
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Phe	Leu	
		35					40					45				

atc	tat	ggg	gta	tcc	agc	agg	gcc	act	ggc	atc	cca	gac	agg	ttc	agt	192
Ile	Tyr	Gly	Val	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser	
	50					55					60					

ggc	agt	ggg	tct	ggg	aca	gac	ttc	act	ctc	acc	atc	agc	aga	ctg	gag	240
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	
65				70					75					80		

cct	gaa	gat	ttt	gca	gtg	tat	tac	tgt	cag	cag	tat	ggg	agt	tca	ccg	288
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro	
				85				90						95		

tgg	acg	ttc	ggc	caa	ggg	acc	aag	gtg	gaa	atc	aaa	cga				327
Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg				
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Glu	Arg	Val	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Arg	Val	Ser	Asn	Ser
			20					25					30		

Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Phe	Leu
		35					40				45				

Ile	Tyr	Gly	Val	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50					55					60				

Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65				70					75					80	

Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro
				85				90						95	

Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105				

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